

[illegible]

RESULT 2

T21498

hypothetical protein F28D1.9 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000

C:Accession: T21498

R:Baynes, C.

submitted to the EMBL Data Library, April 1996

A:Reference number: Z19430

A:Accession: T21498

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-650 <WIL>

A:Cross-references: EMBL:Z70684; PIDN:CAA94602.1; GSPDB:GN00022; CESP:F28D1.9

A:Experimental source: clone F28D1

C:Genetics:

A:Gene: CESP:F28D1.9

A:Map position: 4

A:Introns: 55/2; 87/2; 120/3; 187/1; 241/1; 356/1; 395/1; 600/1

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate-CoA

F:123-609/Domain; acetate--CoA ligase homology <ACLI>

Qy	414	YPRLRVNEDTWELIRGPGVCIPCGEPGQVLGRIIQKDPLRRDFGVLNQCANKKI	473
Db	417	HPVLRIKVDVDTGEAIFSTDGLCIACIPGSGAMVSTIRKNPNLQPEGVLNKKETNKKI	476
Qy	474	AKDVFKKGDAQYTGDVLVMDLGYLFDRDTGDFRWKGENVSTTEVEGTLRLLDMA	533
Db	477	IRDVFAKGDSCFTGLDLHWDLRGYVYFKDRTGDFRWKGENVSTTEVEAILHPITGLSD	536
Qy	534	VAVYGVVEPVTGREGAGMAAVASPTGNCD-----LERRAQVLEKELPLYARPIFLRLPEL	588
Db	537	ATVYGVSVPEQREGVGMASVYVVSHEEDTFQVHRVGARLASSLTSTAIYQPMRQCQDV	596
Qy	589	HKTGYTFQFTELRKEGFDPAIVKDPFLFYLDAAQGRYVPLDQEAYSIQAG	639
Db	597	EKTCTFLVKTNLQRLGIMDA-PSDSIIYVNSENRNEVPFDNDLRCKVSLG	646

RESULT 3
 Tl5879
 hypothetical protein D1009.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
 C:Accession: Tl5879
 R:Favellio, T.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of *C. elegans* cosmid D1009.
 A:Reference number: Z18422
 A:Accession: Tl5879
 A:Status: preliminary; translated from GR/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-655 <FAV>
 A:Cross-references: EMBL:U40938; NID:g1072169; PID:g1072173; PIDN:AAA81698.1; CESP:D1009.1
 C:Genetics:
 A:Gene: CESP:D1009.1
 A:Introns: 2/2; 60/2; 89/3; 125/3; 192/1; 344/2; 399/1; 547/3; 569/3; 602/1
 C:Superfamily: *Mycobacterium tuberculosis* probable fadD6 protein; acetate--CoA ligase
 C:198-611/Domain: acetate--CoA ligase homology <AC1>

Query Match	38.24;	Score	1292;	DB	2;	Length	650;
Best Local Similarity	41.8;	Pred. No.	1.2e-97;				
Matches	272;	Conservative	123;	Mismatches	228;	Indels	28;
Gaps	10;						
Qy	7	LVGVLFSKLVL--KLPTQVGFSLFLYLGSGGWRFRIVFIKTRDIFGGVLVLKVKKA	64				
Db	6	LVTVMLLTAVTAQNPLPGTVILAGVLLIYITVWGDFIYRSLYTLNLRDLTGLALIIIEVKI	65				
Qy	65	KVRQIQEQRRTVPILFASVTRRHPDKTALIFEGTDTHTWTRQLDDEYSSSVANFQAQRIA	124				
Db	66	DLAWRLRHQNGIHELFDLIVKKNPKPAMIDIETNTTVAEFNAHCNRYANFYQGLGYR	125				
Qy	125	SGDVAALFMENRNFVGLWGLMAKLGVAALINLNRDALLHCLLTSRARALVFQSEMA	184				
Db	126	SGDVAALYMSNEFVAAWMLGAKIGVYTAWINLNRQGLVHCITASKTKAIIITSVTLQ	185				
Qy	185	SAICEVHASIDPSL-----SLFCSGSWEP---GAVPSTPEHLDPILKDAKHPKPCPK	235				
Db	186	NIMLD---AIDQKLPDVEGIEVYSGV---EPKKNSGFNKAKKLDQAIIITEPKTLDIV---	237				
Qy	236	GFTDKLFYIYTSGTTGLPKRAALVHVSRYRMAALVYGFMRPNNDIYVDCPLYPHSGAGNI	295				
Db	238	DFKSILCFIYTSGTTGMPKAAVWKHFRYYSIAVGAAGKSFGRPSDRMYVSMPIYHTFAAGI	297				
Qy	296	VTGCQCLLGHMTWIRKFSASRFWDDCIKYNCTIVQYIGELCYRLNPPREANOHQV	355				
Db	298	LGVQALLGGSCVIRKFSASFNFWRDVCVYDQIVSQYIGEICRYLQAQVVEESRHK	357				
Qy	356	RMAIENGRLQROSTWTFNSRFRHPIQVAEYFYGATECNCSLGNFDSQVQACGF---NSRILSFV	413				
Db	358	RILVAGRLAEFTWOPEDRFRY-RIGELYGTSTGSSILVNIIDGHVAGAGFLPSPLTKKM	416				

Db 430 RATGELERDKNGLVCPVCPGCTGEMGVVKEKIDLLKFBGYVSEGDTAKKIYRDFVKHGD 489
QY 483 QAYLTGDLVMDLGLYLFDRDTRFRWKGENVSTTEVEGTLRSRLDMADVAVGVVEVP 542
Db 490 KVFASGDILHWDGLGLYFVDRDGTFRWKGENVSTTEVEGTLQPMVEDATVYGVTVG 549
QY 543 GTEGRAGMAVASPTGNCLEDFE---AQVLEKELPYARPIFLRLPELHKTGYKFKOK 598
Db 550 KMEGRAGMAGIVVKDGT-DVEKEIADITSRLTENLASIALPFIURCKEVDRTGTFKLKK 608
QY 599 TELRKEGFDPAIVK-DPLFYLDQAQGRYVPLDQAYSRIOAG 639
Db 609 TDLQKQGLVACKGDPPIYWSAAEKSYKPLTDKMQOODITG 650

RESULT 4

JW0107

very-long-chain acyl-CoA synthetase related protein - mouse

N:Alternate names: VIAGSR

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Sep-2000

C:Accession: JW0107

R:Berger, J.; Truppe, C.; Neumann, H.; Forss-Petter, S.

Biochem. Biophys. Res. Commun. 247, 255-260, 1998

A:Title: A novel relative of the very-long-chain acyl-CoA synthetase and fatty acid tran-

sferase

A:Reference number: JW0107; MUID:98308102

A:Accession: JW0107

A:Molecule type: mRNA

A:Residues: 1-689

A:Cross-references: GB:AJ223959

A:Experimental source: liver

C:Comment: This protein likely functions as a plasma membrane transporter of long chain

cids.

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase ho-

F:169-647/Domain: acetate--CoA ligase homology <ACL>

Query Match 28.8%; Score 974; DB 1; Length 689;
Best Local Similarity 37.2%; Pred. No. 1.5e-71;
Matches 251; Conservative 104; Mismatches 260; Indels 60; Gaps 18;

QY 1 MLIGASLVGVLLSKVLKLPW-----TQVGFSLFLYL-----GSGGWRFRIRVFTK 48
Db 43 VLLGLALLG-----RPWISSMPPHWSLVGAAULTFLPLQPPPLRLHDKDAV 92
QY 49 IRRDIFGLVLLKVKAKVQCQIERTVPILFASVRRH---PDKALIFEGTD-TWHT 103
Db 93 TFRMLFYGL-----KFRRLNKH---PPETFDALERQALWPRDVALVCTGSGSSIT 143
QY 104 FROLDEYSSSVANFQARGIAGS-----DVAALFM--ENRNEFVGLMGLMAKLGVAAAL 155
Db 144 NSQLDARSQAAWLVKAK-LKDAVIONTRDAAAAILVLPSTISALSVELGLAKLGPVAV 202
QY 156 INTNLRDALLHCLTTSRARALVFGSEMASAICEVHAS-LDPSLSLFCSGSEWEPVAPS 214
Db 203 INPHSGMFLHSHVRSQASVLIVDPDQENLEELVPLKLAENHCFYLGHSPP---TPG 259
QY 215 TEHLDPDLLKADAPKHLPCDPKGFTDK-----LFYIVTSGTGLPKAAIVVHRSRYRMA-AL 269
Db 260 VEALGASLDAAPSD-PVPASLRATIKWKSFAIFTSGTGLPKALLSHERVIOVSNVL 318
QY 270 VYFGFRMRNDIVDCLPLYHSAGNIVIGQCLLHGMVTVIRKKSASRFNDDCIKYNCT 329
Db 319 SFCG--CRADDVVYDVLPIYHITGLVFLGCLQVGCATCVLAPKFSASRFAECRQHGVT 376
QY 330 IVQYIGELCRYLLNOPPREAENQHVMAIENGLRQSIWTFNSSFHPIQVAFFGATEC 389
Db 377 VILYGEILRYLCNWEQPEDKIHIVRLAMGNGLRANVWKNFQRPGRPIRIWEFYGTEG 436
QY 390 NCSLGNFDSQVGCAGFNSRILSFVYPIRLVVRNEDTMELIRPDGVCIPCPGEPGLQV 449
Db 437 NVGLMNVYCHCGAVGTSILRLMIFPFVQFDIETAEPLRDKQFCIPVPEGKGLLIT 496

QY 450 RIIQKDPRLRRDGYNYQGNANKKIADKVKFKGQDAYITGDLVMDLGLYLFDRDGTGTF 509
Db 497 KYRKNQPPFLGVRG--SQAESNRKLVANVRVGDLYFNFTGDLVTLQDQEGFFVQDRLGDTF 554
QY 510 RWKGNVSTTEVEGTLRSRLDMADVAVGVVEVPCTEGRAGMAAV-ASPTGNCLEDERFAOV 568
Db 555 RWKGNVSTGEVESVLSLDFLEEVNVTGVVPGCEGKVGMAAVKLAPGKTFDQGLIYQH 614
QY 569 LEKELPYARPIFLRLPELHKTGYTFQKTELKKEGFDPAIVKDPFLFYLDQAQGRYVPL 628
Db 615 VRSWLPAYATPHFIRIODSLEITNTYKLVKSLRVREGFDVGIADPLVILDNKAQTFRSL 674
QY 629 DOEAYSRIQAGEEKL 643
Db 675 MPDVTQAVCEGTWKL 689

RESULT 5

H83284

probable very-long-chain acyl-CoA synthetase PA2893 [imported] - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83284

R:Stover, C.K.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L-

adman, S.; Yuan, Y.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa-

thogen

A:Reference number: A82950; MUID:20437337

A:Accession: H83284

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-608 <STO>

A:Cross-references: GB:AE004715; GB:AE004091; MID:99948977; PIDN:AAG06281.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2893

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase

Query Match 27.1%; Score 918.5; DB 2; Length 608;
Best Local Similarity 38.2%; Pred. No. 4.4e-67;
Matches 218; Conservative 86; Mismatches 229; Indels 37; Gaps 14;

QY 85 RHDPDKTALIFEGTDTHWTFRQLDEYSSSVANFLOARGLASGDVAAAFMENRNEFVCLWL 144
Db 53 RLYPDNFA-VLDG--QRRISTALFNWANRLARAFKASGVGHGVSVAVMLENRVVELLAILA 110
QY 145 GMAKLGVAAALINTNLRDALLHCLTTSRARALVFGSEMASAICEV-HASLDPSLSLFCFS 203
Db 111 ALAKLGAIGALVNTQGRKVLVHSLNLVKPGHFVVGEELEVEFVEVRHVLGNAGHCY-- 168
QY 204 GSW-----EPGAVPSPSTEHLDPILK-DAPKHLPCSDPKGFTDKLFYIYTSGTGLPK 254
Db 169 --WYDDGDTLDGPGSPPMGRNMLRLAQGQTSNLEDTGRVRLKDSCFYIYTSGTGLPK 226
QY 255 AAVVHSRYR-MAALVYGYFRMRPNDIVDCLPLYHSAGNIVGIGCLLHGMVTVIRKK 313
Db 227 ASIMSHGKWIKAYGGFSGHGLGDRDVLTLPLCYHNNAVTVCSAALAGGAMALRRK 286
QY 314 FSASRFNDDCIKYNCTIVQYIGELCRYLLNOPPREAENQHVMAIENGLRQSIWTFNFS 373
Db 287 FSASGKWDQVQYRATCFYIGELCRYLLNOPPCAEERGNLSLTCMIGNGLRPSIWAFFKQ 346
QY 374 RFHPIQVAFFGATEC---CSLGNFDSQVGCAGFNSRILSFVYPIRLVVRNEDTMELIR 430
Db 347 RFEQRIITEFVASSEGNIPTNFVFNFTV---GFSPTIYA-----IVRYDLENDRPVR 397
QY 431 GPDGVCIPCPGEPGLQVGRITQIKDPLRRPDGYLYNQGNANKKIADKVKFKGQDAYITG 490
Db 398 DAKGFMEKVGKGVGLLILSEISAKWP---PDGYTDPKASEAVILROVFKKGDWAFNTGD 453
QY 491 LVMDLGLY--FRDRTGDTFRWKGENVSTTEVEGTLRSRLDMADVAVGVVEPGTEGRA 548

Db 537 PKLVEFRDELPKSAVGKILRRVLREE 562

RESULT 12

H85484

probable crotonobetaine/carnitine-CoA ligase caic [imported] - Escherichia coli (strain C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: H85484

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, J.; Miller, L.; Grothbeck, E.J.; Davis, N.W.; Llim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H85484

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-522 <STO>

A:Cross-references: GB:AE005174; NID:q12512724; PIDN:AAG54340.1; GSPDB:GN00145; UWGP:Z00

A:Experimental source: strain O157:H7 [substrain EDL933

C:Genetics: caic

C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

Query Match 10.9%; Score 369.5; DB 2; Length 522;

Best Local Similarity 24.6%; Pred. No. 3 5e-22;

Matches 140; Conservative 85; Mismatches 273; Indels 71; Gaps 18;

Db 52 DIFGGLVLLKAKVROCIQERTVPILFASVVRHDPKTLIFE---GTDTHWTFRLQD 108

Db 7 DIIGG-----QHLRQMMDLADV-----YGHKTALICESGGVWNRYVLELN 49

Db 109 EYSSVANFLQARGLASGVDAIFMENRNEFFVCLWLGMAKLGVEALINTNRRDALLHC 168

Db 50 QETNRANFYTGIRKQDKVALHLDNCPETFCFGLAKIGAIMVPIINARLLREESAWI 109

Db 169 LTTSRALVFGSEMAISAICEVHASLDPSLSFCSGSWEPGAVP--PSTEHLDPILKQAP 226

Db 110 LQNSQACLLVTSQAQFPMYQIQEDATQLRHIC---LTDVALPADDGVSSFTQLKNQOP 166

Db 227 KHLPCSPDKGFTDKLYIYTSGTGLPKAAIVVHSRYRMAALVYVG---FMRMRNDIYV 283

Db 167 ATLCAAPPLSTDDTABILFTSGTTSRPGKGVITH---YNLRFAGYYSAWQCALRDDVVYL 223

Db 284 DCLPLYHSAGNIVGICQLLHGMVTVIRKKFSASRFWDDCIKYNCTIVYIGELCRYLLN 343

Db 224 TVMPAFHIDCOCTAANAASFAGATFVLVEKYSARAFWGVQVYRATIEICPMMLITLMV 283

Db 344 QPPREAHQHVRLMAGN-GLRQSIWTFNSRPHIPQVAEFTGATECNCS-LGNFDS--- 398

Db 284 QPPSANDRQHLREVFMVYLNSEQEKDTFCERFGV-RLTTSYGMTETIVGIIIGDRPGDKR 342

Db 399 ---QVACAGCNSILSFVPIRLVRVNETMELIRGPDG-VCIPOCPGPGGLVRIIOK 454

Db 343 RWSIGRAGF-----CYDAEIR-----DDHNRPLPAGEIGEICI---KGVPGKTIFF--- 386

Db 455 DPLRRFDGVLNOCANNKKAIVKFGDQAYL-TGDLVLMDELGYLFRDRDTGDFRWMKG 513

Db 387 -----EYFLNPKATAKVLAD-----GWLHTGDTGYRDEGFFYFIDRCNMIRKGG 433

Db 514 ENVSTTEVEGTLSRLDMDADVGVVEVPGTEGRAGMAAASVPTGNCDLERFAQVLEKEL 573

Db 434 ENVSCVLENIATHPKIDIVVVGKIDSRDEAIFAKFVVLNEGETLSEEFCEQNM 493

Db 574 PLYARFELRLPELHKTKTYKFKTEL 602

Db 494 AKFVPSYLEIRKDLPRNCSGKILRNKLK 522

RESULT 13

A69831

probable acid--CoA ligase (EC 6.2.1.-) yhfL [similarity] - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: A69831

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Ehrlich, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Brouillet, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gal tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadaie, V.; Sato, T.; Scapli A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se keuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis A:Reference number: A69580; MUID:98044033

A:Accession: A69831

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-513 <KUN>

A:Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12867.1; PID:g26333

A:Experimental source: strain 168

C:Genetics: yhfL

C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

C:Keywords: acid-thiol ligase

F:47-507/Domain: acetate--CoA ligase homology <ACL>

Query Match 10.8%; Score 364.5; DB 2; Length 513;

Best Local Similarity 26.8%; Pred. No. 8.7e-22;

Matches 144; Conservative 67; Mismatches 270; Indels 57; Gaps 16;

Db 83 TVRRHPDKTALIFEGTDHTFROLDEYSSVANFLQARGLASGVDAIIFMENRNEFVGL 142

Db 10 TASEKPDIAICRFK--DHMTYQELNEYIQRFADGLEAGKEGHDHALLLGNSPDIIIA 67

Db 143 WLGMAKLGVEAALINTNRRDALLHCLTTSRARALVFGSEMAISAICEVHASLDP-SLSLF 201

Db 68 FFGALKAGIVVVPINPLYTPTEIGYMLTNGDVKAIVGVSQLLPLLYESMHESLPKVELVIL 127

Db 202 C-SGSWEPAVPS-----TEHLDPLKADAPKPLSPDKGFTDKLFVYTSGTGL 252

Db 128 CQTEAEPEADPEVRKMTTFKILRP-TSAAKQNEPVPD----DTAVLITSGTIGK 182

Db 253 PKAAIVHSRYRMAALV--TYGFRMRPNDIVDCLPLYHSAGNIVGICQLLHGMVTVI 310

Db 183 PKGAMLTNOLYNSANDVAGYLGMDERDN--VVCALPMCHVFCLTVCNNAPLMSGATVLI 240

Db 311 RKKSASRFWDDCIKYNCTIVYIGELCRYLLNQPPREAHQHVRLMAGN--LRQSIW 368

Db 241 EPQSPASVFLKVRQQQATIFAGVPTMYNLFQHENGKDDFSIRLCISGGASMPVALL 300

Db 369 TNSRRPHIPOVAEFGATECN--CSLGNED--SQVACGCFNSRLSFVYPIRLVRVNE 424

Db 301 TAFEKFGV-TILEGYLSEASPTCFNPDGRKPGSIG----- 339

Db 425 TMELIRGPDGVCIPQCPGPGQLVGRITQKDPRLRRFQGYLNOGANNKKAIAKDFKKGQDA 484

Db 340 -TSILHVENKVVDPLGRELPAHQVGLIVKGP-NVMKGYKMPMETEHALKDGW----- 391

Db 485 YLTGDVLMDELGYLFRDRDTGDFRWMKGENVSTTEGILSRLLDMADVAVYGVVEPVT 544

Db 392 LYTGDLARREDGEGYFIYVDRKKDIIIVGGYNYVPREVEEVLISHPDYKEAVTIGVDPD-Q 450

Db 545 EGRAGMAAVASPTGNCDLERFAQVLEKELPLYARPIFLRLPELHKTKTYKFKTEL 602

Db 451 SGEAVGVVVPKRSVTEEDINQCEKHLAKYKRPAAITFDDIPKNAKMLRRALR 508

RESULT 14

probable coA ligase - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000
 C:Accession: G70986
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98293987
 A:Accession: G70986
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-532 <COL>
 A:Cross-references: GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CAB09316.1; PID:g2131015
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: fadD1
 A:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
 F:48-499/Domain: acetate--CoA ligase homology <ACL>

Query Match 10.6%; Score 358; DB 2; Length 532;
 Best Local Similarity 24.5%; Pred. No. 3.1e-21;
 Matches 145; Conservative 77; Mismatches 229; Indels 142; Gaps 20;

QY 82 STVRRHPDKTALIFGDTHTWTFRLDYEYSSVANFLQARGLASGDVAAIFMENEFVGF 141
 Db 7 SLRQHVSDPTIAVKGGLQWTSQ-----YLAESARAALITADPQRPHTIG 56
 QY 142 LWLG-----MAKL-----GVRAALINTLNRDAL-----LHC-----LTSRARALVFGS 181
 Db 57 SLGNTPEMLAQLAAAGLVGCLNTRRGDAADVRRADCCQIVVTADHRAALLDGL 116
 QY 182 EMASACEVHASLDPSLFLSCSGSEPGAVPPSTHLDPLLLKADPKHLPSCDKGFTKL 241
 Db 117 DLGA-----RLDSTPRAELVAGDGFVYRE-VDTM-----DPF 153
 QY 242 FYIYTGTTGLPKAAIVHVSRYRMAALVYIGFRMRPNIDVDCPLXHSAGNIGIGQC 301
 Db 154 MLIYTGTTSGNPKAVPVSHLMATFAGRSUTERFGLTEQDTCVSNPLFHSNAVAVAGWAPA 213
 QY 302 LLHGWTWIRKFFESARFDDCIKNTIVQIGELCYLLNQPRAENQHVQRMALGN 361
 Db 214 VVSG-AAIAPATFSATGFLDDVRRVHATYMYVVGKPLAYILATPERDDADNPLRAFGN 272
 QY 362 GLRQSTWTFNSRFRHPOVAEYFQATE-----CN 390
 Db 273 EANDKDIEFSRRFGV-QVEDFGSTENAVIVIREPPTPGSIGRANGVAVNGETVTE 331
 QY 391 CSLGNFDSQVAGCGNSRILSFYPIRLVRVNDTMEILIRGPDGVCIPQGPQGLVGR 450
 Db 332 CAVAREDAH-GAL-----TNAD-----EAIGE 352
 QY 451 IIOKDLPRFDGYLNO-GANNKKIAKDFKGDQAYLITGDVLVMDLGYLFRDRTGDTF 509
 Db 353 LVNTTSGSGFTGYNDPEANEARHGMVYSGDLAY-----RDSEGWYLAGRTADWM 405
 QY 510 RWRGENVSTVEGTLRLDMDADVAVGV--EVPGTGRAGMAVAVSPTGCD-LERFA 566
 Db 406 RVDGENLTAAPIERILLYKAINRVAVYVDPYVGDQVMAALVLRAGDTFDDPAFAFL 465
 QY 567 OVLEKELPLYARPIFLRLPELHKTGTYKFKQTELKKEG-----FDPAAIVKDP 614
 Db 466 DA-QPDLSTKAPRIVIRIADLPSTATHKVLKRLQIDEGTAVGKADTLWVREP 517

RESULT 15

S40558
 probable carnitine--CoA ligase (EC 6.2.1.-) - Escherichia coli

C:Species: Escherichia coli
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: E64724; S40558; I41013
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 .A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: E64724
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-522 <BLAT>
 A:Cross-references: GB:AE000114; GB:U00096; NID:g1786217; PIDN:AACT3148.1; PID:g17862
 A:Experimental source: strain K-12, substrain MG1655
 R:Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Miz
 submitted to the EMBL data library, December 1992
 A:Description: Systematic sequencing of the Escherichia coli genome: analysis of the
 A:Reference number: S40531
 A:Accession: S40558
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-522 <YUR>
 A:Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01313.1; PID:g216462
 R:Eichler, K.; Bourgis, F.; Buchet, A.; Kleber, H.P.; Mandrand-Berthelot, M.A. Mol. Microbiol. 13, 775-786, 1994
 A:Title: Molecular characterization of the cai operon necessary for carnitine metabol
 A:Reference number: I41010; MUID:95115548
 A:Accession: I41013
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-102, 'R', 104-256, 'PR', 259-290, 'R', 292-332, 'S', 334-349, 'A', 351-378, 'V', 38
 A:Cross-references: EMBL:X73904; NID:g563860; PIDN:CAA52113.1; PID:g563864
 A:Experimental source: strain O44 K74
 C:Genetics:
 A:Gene: caiC
 C:Function:
 A:Pathway: lysine degradation; tryptophan metabolism
 C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
 C:Keywords: acid-thiol ligase; ATP; phosphoprotein; transmembrane protein
 F:63-521/Domain: acetate--CoA ligase homology <ACL>
 F:81-97/Domain: transmembrane #status predicted <TM1>
 F:235-251/Domain: transmembrane #status predicted <TM2>
 F:194/Active site: Lys #status predicted

Query Match 10.4%; Score 350.5; DB 2; Length 522;
 Best Local Similarity 24.1%; Pred. No. 1.2e-20;
 Matches 137; Conservative 86; Mismatches 275; Indels 71; Gaps 18;

QY 52 DIFGGLVLLKAKVRQCLQERTVPIPLFASVRRHPDKTALIFE---GTDTHWTFRLD 108
 Db 7 DIIG-----QHLRQWDDLDV-----YGHKTALICESGGVYVNRYSYLELN 49
 QY 109 EYSSVANFLQARGLASGDVAAIFMENEFVGLWLMKAKIGVEAALINTLNRDALLHC 168
 Db 50 QEINTNANLTYTIGIRKGDVKAHLHLDNCPEIFCWFGLAKIGAINVPIVARLLCESAWI 109
 QY 169 LTTSRARALVFGSEMAAICEVHASLDPSLFLSCSGSEPGAVP--PSTHLDPLLLKADP 226
 Db 110 LONSQACLLVTSQAQFPMYQIQOEDATQLRHIC---LTDVALPADDDGVSSFTQLKNOQP 166
 QY 227 KHLPSCKDGKFTDKLFYIYTGTTGLPKAAIVHVSRYRMAALVYIG---FMRPNDIYV 283
 Db 167 ATLCAPIPLSTDDTAELFTSGTTSRPGKGVITH---YNLRFAGYYSAWOALRDDVDYL 223
 QY 284 DCLPLXHSAGNIGIGQCLLHGMVTVIRKFSASREWDCCIKNCTIVQIGELCYLLN 343
 Db 224 TVMPAFHIDCQCTAANAAPASAGATFVLVEXYSARAFGQVQKYRATVETCIPMIRTLAV 283
 QY 344 QPPREANQHVQRMALGN-GLRQSTWTFNSRFRHPOVAEYFQATECNCS-LGNFDS--- 398
 Db 284 QPPSANDQQHRLREVNFYLNLSQEKDAFCERFGV-RLTTSYGMTETIVGIIGDRPGDKR 342

QY 399 ---QVACGNSRITLSEVYPIRLVRVNEIDMELIRGPDG-VCIPCOGPEGQLVGRIOK 454
 Db 343 RWPISGRVGF-----CYEAER---DDHNRPLPAGEIGEICI---KGIPGKTIFK----- 386
 QY 455 DPLRRFDGYLNOGANNKKIAKDVFKKGDQAYL-TGDVLMDELGYLYFRDRTGDTFRWKG 513
 Db 387 -----EYFLNPQATAKVLEAD-----CWLHTGDTGYRDEDEFFVVDRCNMIRKGG 433
 QY 514 ENVSTTEVEGTLSKLLDMADVAVYGVVPGTEGRAGMAAVASPTGNCDLERFAQVLEKEL 573
 Db 434 ENVSCVELENIIAHPKIQIDIVVVGIKDSIRDEAIAKAFVVLNEGTELSEEEFFRCEQNM 493
 QY 574 PLYARPIFLRLPELHKGTGYKFKQTELR 602
 Db 494 AKFKVPSYLEIRKDLPRNCCKIIRNLK 522

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7